

10 30 50
 GTGAGATGGTGGCTTTCATGAATTCCTCCCAACAAGAGCCAAGCTCTCCATCTAGTGGACAG
 70 90 110
 GGAAGCTAGCAGCAAACCTTCCCTTCACTACGAAACTTCATTGCTTGGCCCAAAAGAGAG
 130 150 170
 TTAATTCAATGTAGACATCTATGTAGGCAATTAAAAACCTATTGATGTATAAAACAGTTT
 190 210 230
 GCATTCATGGAGGGCAACTAAATACATTCTAGGACTTTATAAAAGATCACTTTTATTTA
 250 270 290
 TGCACAGGGTGGAACAAGATGGATTATCAAGTGTCAAGTCCAATCTATGACATCAATTAT
 M D Y Q V S S P I Y D I N Y
 310 330 350
 TATACATCGGAGCCCTGCCCAAAATCAATGTGAAGCAAATCGCAGCCCGCCTCCTGCCT
 Y T S E P C P K I N V K Q I A A R L L P
 370 390 410
 CCGCTCTACTCACTGGTGTTCATCTTTGGTGGTGGTGGCAACATGCTGGTCATCCTCATC
 P L Y S L V F I F G F V G N M L V I L I
 430 450 470
 CTGATAAACTGCCAAAGGCTGGAGAGCACTGACATCTACCTGCTCAACCTGGCCATC
 L I N C Q R L E S M T D I Y L L N L A I
 490 510 530
 TCTGACCTGTTTTCTTCTTACTGTCCCTTCTGGGCTCACTATGCTGCCGCCAGTGG
 S D L F F L L T V P F W A H Y A A A Q W
 550 570 590
 GACTTTGGAATACAATGTGTCAACTCTTGACAGGGCTCTATTTTATAGGCTTCTTCTCT
 D F G N T M C Q L L T G L Y F I G F F S
 610 630 650
 GGAATCTTCTTCATCATCCTCCTGACAATCGATAGGTACCTGGCTATCGTCCATGCTGTG
 G I F F I I L L T I D R Y L A I V H A V
 670 690 710
 TTTGCTTTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAGTGTGATCACTTGGGTG
 F A L K A R T V T F G V V T S V I T W V
 730 750 770
 GTGGCTGTGTTTGCGTCTCTCCCAGGAATCATCTTTACCAGATCTCAAAAAGAAGGTCTT
 V A V F A S L P G I I F T R S Q K E G L
 790 810 830
 CATTACACCTGCAGCTCTCATTTTCCATACAGTCAGTATCAATTCTGGAAGAATTTCCAG
 H Y T C S S H F P Y S Q Y Q F W K N F Q
 850 870 890
 ACATTAAAGATAGTCATCTTGGGGCTGGTCTGCCGCTGCTTGTGTCATGGTCATCTGCTAC
 T L K I V I L G L V L P L L V M V I C Y
 910 930 950
 TCGGGAATCCTAAAACTCTGCTTCGGTGTGCAATGAGAAGAAGAGGCACAGGGCTGTG
 S G I L K T L L R C R N E K K R H R A V
 970 990 1010
 AGGCTTATCTTCACCATCATGATTGTTTATTTTCTTCTTCTGGGCTCCCTACAACATTGTC
 R L I F T I M I V Y F L F W A P Y N I V
 1030 1050 1070
 CTTCTCCTGAACACCTTCCAGGAATCTTTGGCCTGAATAATTGCAGTAGCTCTAACAGG
 L L L N T F Q E F F G L N N C S S S N R
 1090 1110 1130
 TTGGACCAAGCTATGCAGGTGACAGAGACTCTTGGGATGACGCACTGCTGCATCAACCCC
 L D Q A M Q V T E T L G M T H C C I N P
 1150 1170 1190
 ATCATCTATGCCTTTGTGCGGGAGAAGTTTCAAACTACCTCTTAGTCTTCTTCAAAAG
 I I Y A F V G E K F R N Y L L V F F Q K
 1210 1230 1250
 CACATTGCCAAACGCTTCTGCAAATGCTGTCTATTTCAGCAAGAGGCTCCCGAGCGA
 H I A K R F C K C C S I F Q Q E A P E R
 1270 1290 1310
 GCAAGCTCAGTTTACACCCGATCCACTGGGGAGCAGGAAATATCTGTGGGCTGTGACAC
 A S S V Y T R S T G E Q E I S V G L *
 1330 1350 1370
 GGACTCAAGTGGGCTGGTGACCCAGTCAGAGTTGTGCAATGGCTTAGTTTTTCATACACA

FIGURE 1A

1390 1410
GCCTGGGCTGGGGGTGGGGTGAAGAGGTCTTTT

10057800.020800

FIGURE 1B

Homology Comparison HDG NR10.Pro x Hu. MCP-1 Receptor

Percent Similarity: 82.991 Percent Identity: 70.088

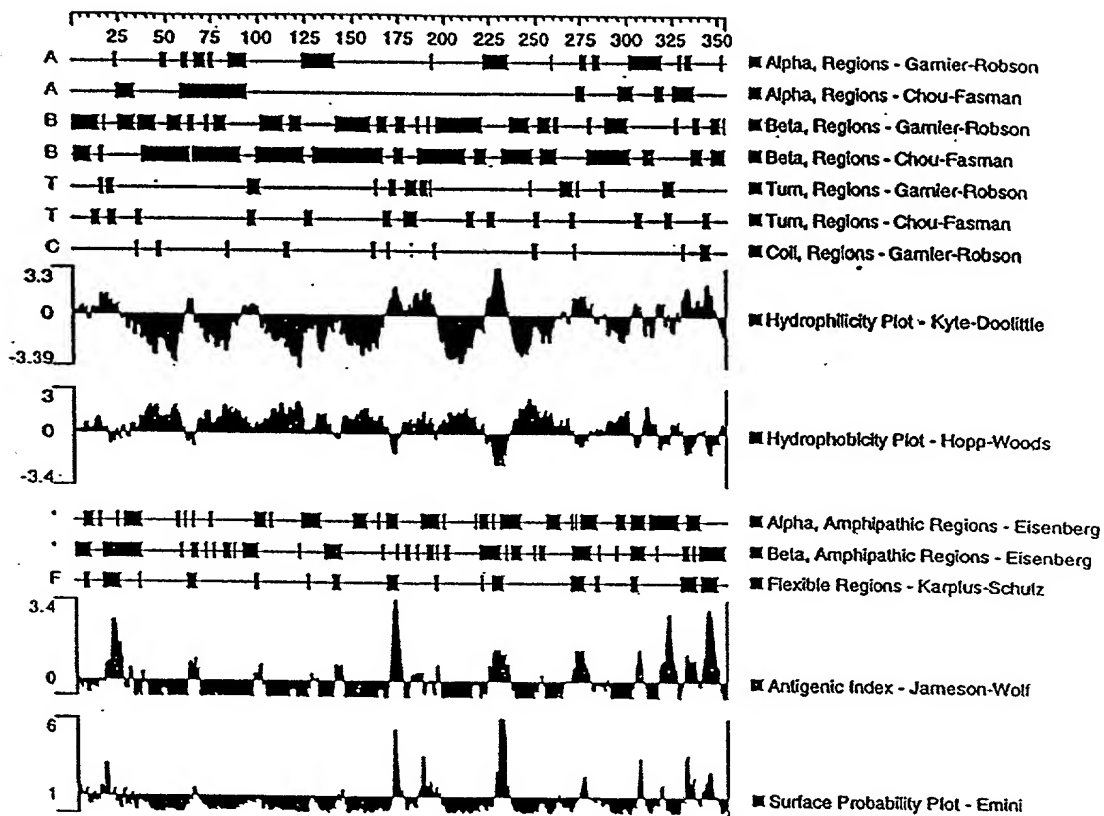
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4 QVSSPIYDINYYTSEPCPKINVKQIAARLLPPLYSLVFIFGFVGNMLVIL 53
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
18 EEVTTFFDYDY . . GAPCHKFDVKQIGAQLLPPLYSLVFIFGFVGNMLVVL 65
54 ILINCQRLESMTDIYLLNLAISSLFLLTVPFWAHYAAAQWDFGNTMCQL 103
| | | | | . . . . . : | | | | | : | | | | | : | | | | | : | | | | |
66 ILINCKKLKCLTDIYLLNLAISSLFLLTLPLWAHSAANEVWVFGNAMCKL 115
104 LTGLYFIGFFSGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITW 153
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
116 FTGLYHIGYFGGIFFIILLTIDRYLAIVHAVFALKARTVTFGVVTSVITW 165
154 VVAVFASLPGLIIFTRSQKEGLHYTCSSHPYSQYQFWKNFQTLKIVILGL 203
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
166 LVAVFASVPGIIFTKQKEDSVYVCGPYFPRG . . . . WNNFHTIMRNILGL 211
204 VLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWAPYNI 253
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
212 VLPLLIMVICYSGILKTLLRCRNEKKRHRAVRVIFTIMIVYFLFWTPYNI 261
254 VLLNNTFQEFFGLNNCSSLNRDQAMQVTETLGMTHCCINPIIYAFVGEK 303
| : | | | | | | | | | | | . | . . . . | | | | | | | | | | |
262 VILLNNTFQEFFGLSNCESTSQLDQATQVTETLGMTHCCINPIIYAFVGEK 311
304 FRNYLLVFFQKHIAKRFCKCCSIFQQEAPERASSVYTRS . . . TGEQEISV 350
| | . . . : . . : | | . . . | . . . | | . . . : . . : |
312 FRSLFHIALGCRIA . PLQKPVCGGPGVRPGKNVKVTTQGLLDGRGKGKSI 360
351 G 351
361 G 361

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FIGURE 2

Figure 3



10067800 020600

Anti-CCR 5 1D8 VH Sequence

1 CAGGTGCAGCTGCAGGAGTGGGGCCAGGACTGGTGAAGCCTTGGGAGAACCTGTCCCTC
1 Q V Q L Q E S G P G L V K P S E T L S L
61 ACCTGCACTGTCCTCTGGTGGCTCCATCAGTAGTTTCTACTGGAGCTGGATCCGGCAGCCC
21 T C T V S G G S I S S F Y W S W I R Q P
121 GCCGGGAAGGGACTGGATTGGGCGTATCTATAACCAGCGGGAACAACCAACTACAAC
41 A G K G L D W I G R I Y T S G N T N Y N
181 CCTCCCTCAAGAGTCAAGTACCATGTCAAGTACACGTCCTCAAGAACCGGTTCCTCCCTG
61 P S L K S R V T M S V D T S K N R F S L
241 AAACCTGAGCTCTGTGACCGCCGGGACACGGCCGTGTATTACTGTGGGAGA GATCGGGGC
81 K L S S V T A A D T A V Y Y C A R D R G
301 AGCAGCTGGTACCCCGATGCTTTTGATATCTGGGGCCAAAGGACAATGGTCAACGCTCTCC
101 S S W Y P D A F D I W G Q G T M V T V S
361 TCA
121 S

Anti-CCR 5 1D8 VK Sequence

1 GATATTGTGTGACGCACTCTCCAGGCACCCCTGTCTTTGTCTCTCCAGGGGAAAGAGGCCACC
1 D I V L T H S P G T L S L S P G E R A T
61 CTCCTCTGCAGGGCCAGTCAAGGTGTACAGCAGCTGCTTAGCCTGGTACCAGCAGAAA
21 L S C R A S Q R V T S S C L A W Y Q Q K
121 OCTGGCCAGGCTCCAGGCTCTCATCTATGGTACATCCAGCAGGGGCCACTGGCATCCCA
41 P G Q A P R L L I Y G T S S R A T G I P
181 GACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAG
61 D R F S G S G S G T D F T L T I S R L E
241 OCTGAAGATTTTGCAGTGTATTACTGTGAGCAGTATGTTAGCTCACCTCTCACCTTCGGC
81 P E D F A V Y Y C Q Q Y V S S P L T F G
301 CAAGGGACACGACTCGAGATCAAAAGT
101 Q G T R L E I K R

FIG. 4

Anti - CCR5 3C9 VH

1 GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTA AAG TCT GGG GGG TCC CTT AGA CTC 60
1 E V Q L V E S G G G L V K S G G S L R L 20

CDR1

61 TCC TGT GCA GCC TCC GGA TTC ACT TTC AGT AAC GCC TGG ATG ACC TGG GTC CGC CAG GCT 120
21 S C A A S G F T F S N A W M T W V R Q A 40

CDR2

121 CCA GGG AAG AGG CTG GAG TGG GTT GGC CGT ATT AAA AGC AAT GCT GAT GGT GGG TCA ACA 180
41 P G K R L E W V G R I K S N A D G G S T 60

181 GAC TAC GCT GCA CCC GTG AAA GGC AGA TTC ACC ATC TCA AGA GAT GAT TCA AAA AAC ACG 240
61 D Y A A P V K G R F T I S R D D S K N T 80

241 CTG TAT CTG CAA ATG AAC AGC CTG AAA ACC GAG GAC ACA GCC GTG TAT TAC TGT AAC ACA 300
81 L Y L Q M N S L K T E D T A V Y Y C N T 100

CDR3

301 GAT AAG GGT GGG AGC TAC CCC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGG ACC 360
101 D K G G S Y P Y Y Y Y G M D V W G Q G T 120

361 ACG GTC ACC GTC TCC TCA G 379

121 T V T V S S 127

Anti-CCR5 3C9 VK

1 GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC 60
1 D I Q M T Q S P S S L S A S V G D R V T 20

CDR1

61 ATC ACT TGC CGG GCA AGT CAG GGC ATT AGA AAT GAT TTA GGC TGG TAT CAG CAG AAA CCA 120
21 I T C R A S Q G I R N D L G W Y Q Q K P 40

CDR2

121 GGG AAA GCC CCT AAG CGC CTG ATC TAT GAT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA 180
41 G K A P K R L I Y D A S S L Q S G V P S 60

181 AGG TTC AGC GGC AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGC CTG CAG CCT 240
61 R F S G S G S G T E F T L T I S S L Q P 80

CDR3

241 GAA GAT TTT GCA ACT TAT TAC TGT CTA CAG CAT AAT AGT TAC CCA TTC ACT TTC GGC CCT 300
81 E D F A T Y Y C L Q H N S Y P F T F G P 100

301 GGG ACC AAA GTG GAT ATC AAA CGA 324

101 G T K V D I K R 108

Fig. 5

Anti-CCR5 9E6 VH

1 GAG GTG CAG CTG GTG GAG TCT GGC CCA GGA CTG GTG AAG CCT TCG GAG ACC CTG TCC CTC 60
1 E V Q L V E S G P G L V K P S E T L S L 20

CDR1

61 ACC TGC ACT GTC TCT GGT GGC TCC ATC AGT AGT TAC TAC TGG AGC TGG ATC CGG CAG CCC 120
21 T C T V S G G S I S S Y Y W S W I R Q P 40

CDR2

121 CCA GGG AAG GGA CTG GAG TGG ATT GGG TAT ATC TAT TAC AGT GGG AGC ACC AAC TAC AAC 180
41 P G K G L E W I G Y I Y Y S G S T N Y N 60

181 CCC TCC CTC AAG AGT CGA GTC ACC ATA TCA GTA GAC ACG TCC AAG AAC CAG TTC TCC CTG 240
61 P S L K S R V T I S V D T S K N Q F S L 80

241 AAG CTG AGC TCT GTG ACC GCT GCG GAC ACG GCC GTG TAT TAC TGT GCG AGA GAT GTC ATG 300
81 K L S S V T A A D T A V Y Y C A R D V M 100

CDR3

301 CAG CAG CCG GTA CCG GGT TAC TAC TAC TAC TAC GGT ATG GAC GTC TGG GGC CAA GGA ACC 360
101 Q Q P V R G Y Y Y Y Y G M D V W G Q G T 120

361 CTG GTC ACC GTC TCC TCA 378

121 L V T V S S 126

Anti-CCR5 9E6 VK

1 GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GTC ACC 60
1 E I V L T Q S P G T L S L S P G E R V T 20

CDR1

61 CTC TCC TGC AGG GCC AGT CAG AGA GTT AGC AAC AGC TAC TTA GCC TGG TAC CAG CAG AAA 120
21 L S C R A S Q R V S N S Y L A W Y Q Q K 40

CDR2

121 CCT GGC CAG GCT CCC AGG TTC CTC ATC TAT GGT GTA TCC AGC AGG GCC ACT GGC ATC CCA 180
41 P G Q A P R F L I Y G V S S R A T G I P 60

181 GAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG 240
61 D R F S G S G S G T D F T L T I S R L E 80

CDR3

241 CCT GAA GAT TTT GCA GTG TAT TAC TGT CAG CAG TAT GGT AGT TCA CCG TGG ACG TTC GGC 300
81 P E D F A V Y Y C Q Q Y G S S P W T F G 100

301 CAA GGG ACC AAG GTG GAA ATC AAA CGA 327

101 Q G T K V E I K R 109

Fig. 6